

960296_99004_Seq_Lst
SEQUENCE LISTING

```

<110>  Chapman, Edwin R.
        Dong, Min

<120>  BOTULINUM NEUROTOXIN B RECEPTORS AND USE THEREOF

<130>  960296.99004

<140>  10/695,577
<141>  2003-10-28

<150>  60/422,951
<151>  2002-10-31

<150>  60/498,128
<151>  2003-08-27

<160>  10

<170>  PatentIn version 3.3

<210>  1
<211>  2381
<212>  DNA
<213>  Mus musculus

<220>
<221>  CDS
<222>  (525)..(1790)

<220>
<221>  misc_feature
<222>  (618)..(680)
<223>  BoNT/B binding domain

<220>
<221>  misc_feature
<222>  (681)..(761)
<223>  Gangliosides binding domain or transmembrane domain

<400>  1
accggggcaa gccccaggg tcctgctcac ccaacagggg gctcaggtcc ccgaagtgtg      60
tgcagggcgg gggcggccag ctgggaccag ctggtggccc tagaaaacct caccacacc      120
cacaccaca caccctttt gtgttgagg ctgcccctct gagagcggag gcagcgagag      180
agtactcgtt tgcctcgcac cggtcgcgg tgagagcagc ggggaccaag actcgcacca      240
tctcccggtc ggtcctcgct ccagtttccc tctgaatcct acacttcata tgtagacacc      300
ttactcaact ggcatttggt agtcaagtct cctctgcata caaggaaaag aagacttttg      360
cgcgctcgaa caaccaacat aagcagtctg atcagaagac attcaaattg ccgtcccagag      420
agctccagca gaacatctcg ttaagattga agaaaggaga ttccaaaagg acaaaaaacc      480
caaatactcc agactacccc cagcagacat ccgctgaacc aaaa atg gtg agt gcc      536
                                   Met Val Ser Ala
                                   1

```

960296_99004_Seq_Lst

agt Ser 5	cgt Arg	cct Pro	gag Glu	gcc Ala	ctg Leu 10	gct Ala	gcc Ala	cct Pro	gtc Val 15	acc Thr	act Thr	gtt Val	gcg Ala	acc Thr	ctt Leu 20	584
gtc Val	cca Pro	cac His	aac Asn 25	gcc Ala	act Thr	gag Glu	cca Pro	gcc Ala	agt Ser 30	cct Pro	ggg Gly	gaa Glu	ggg Gly	aag Lys 35	gaa Glu	632
gat Asp	gcc Ala	ttt Phe	tcc Ser 40	aag Lys	ctg Leu	aag Lys	cag Gln 45	aag Lys	ttt Phe	atg Met	aat Asn	gaa Glu 50	ctg Leu 50	cat His	aaa Lys	680
atc Ile	cca Pro	ttg Leu 55	cca Pro	ccg Pro	tgg Trp	gcc Ala 60	tta Leu	att Ile	gcc Ala	ata Ile	gcc Ala 65	ata Ile	gtt Val	gcg Ala	gtc Val	728
ctt Leu 70	cta Leu	gtc Val	gtg Val	acc Thr	tgc Cys	tgc Cys 75	ttc Phe	tgt Cys	gtc Val	tgt Cys	aag Lys 80	aaa Lys	tgt Cys	ttg Leu	ttc Phe	776
aaa Lys 85	aag Lys	aaa Lys	aac Asn	aag Lys	aag Lys 90	aag Lys	gga Gly	aag Lys	gaa Glu 95	aag Lys 95	gga Gly	ggg Gly	aag Lys	aac Asn	gcc Ala 100	824
att Ile	aac Asn	atg Met	aaa Lys	gac Asp 105	gtg Val	aaa Lys	gac Asp	tta Leu	ggg Gly 110	aag Lys	acc Thr	atg Met	aag Lys	gat Asp 115	cag Gln	872
gcc Ala	ctt Leu	aag Lys	gat Asp 120	gac Asp	gat Asp	gct Ala	gaa Glu	act Thr 125	gga Gly	ctg Leu	act Thr	gat Asp	gga Gly 130	gaa Glu	gaa Glu	920
aag Lys	gag Glu	gag Glu 135	ccc Pro	aag Lys	gaa Glu	gag Glu	gag Glu 140	aaa Lys	ctg Leu	gga Gly	aag Lys	ctt Leu 145	caa Gln	tat Tyr	tca Ser	968
ctg Leu 150	gac Asp	tat Tyr	gac Asp	ttc Phe	cag Gln	aat Asn 155	aac Asn	cag Gln	ctg Leu	ctg Leu	gtg Val 160	gga Gly	atc Ile	atc Ile	cag Gln	1016
gct Ala 165	gct Ala	gaa Glu	ctg Leu	ccc Pro	gcc Ala 170	ctg Leu	gac Asp	atg Met	gga Gly	ggc Gly 175	aca Thr	tct Ser	gat Asp	cca Pro	tac Tyr 180	1064
gtc Val	aaa Lys	gtc Val	ttc Phe	ctg Leu 185	ctg Leu	ccc Pro	gac Asp	aaa Lys	aag Lys 190	aag Lys	aag Lys	ttt Phe	gag Glu	aca Thr 195	aaa Lys	1112
gtc Val	cac His	cgg Arg	aaa Lys 200	acc Thr	ctc Leu	aat Asn	cca Pro	gtc Val 205	ttc Phe	aat Asn	gaa Glu	cag Gln	ttt Phe 210	act Thr	ttc Phe	1160
aag Lys	gtg Val	cca Pro 215	tac Tyr	tcg Ser	gaa Glu	tta Leu	ggt Gly 220	ggc Gly	aag Lys	aca Thr	ctg Leu	gtg Val 225	atg Met	gct Ala	gtg Val	1208
tat Tyr	gat Asp 230	ttt Phe	gac Asp	cgc Arg	ttc Phe	tcc Ser 235	aag Lys	cac His	gac Asp	atc Ile	att Ile 240	gga Gly	gag Glu	ttc Phe	aaa Lys	1256
gtt Val 245	cct Pro	atg Met	aac Asn	acc Thr	gtg Val 250	gat Asp	ttt Phe	ggc Gly	cac His	gtc Val 255	acc Thr	gag Glu	gag Glu	tgg Trp	cgc Arg 260	1304

960296_99004_Seq_Lst

gat ctc cag agt gct gag aaa gaa gag caa gag aaa ctg ggt gac atc Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys Leu Gly Asp Ile 265 270 275	1352
tgc ttc tcc ctc cgc tac gtc cct act gcc ggc aag ctg act gtt gtc Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr Val Val 280 285 290	1400
att ctg gaa gcc aag aac ctg aag aag atg gat gtg ggt ggc tta tct Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly Leu Ser 295 300 305	1448
gat ccc tat gta aag att cac ctg atg cag aac ggc aag aga ctg aag Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly Lys Arg Leu Lys 310 315 320	1496
aag aaa aag aca acg att aag aag aac aca ctt aac ccc tac tac aat Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn 325 330 335 340	1544
gag tcc ttc agc ttt gaa gtt ccg ttc gag caa atc cag aaa gtg caa Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile Gln Lys Val Gln 345 350 355	1592
gtg gtg gta act gtt ttg gac tat gac aag att ggc aag aac gac gcc Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala 360 365 370	1640
atc ggc aaa gtc ttt gtg ggc tac aac agc acc ggc gca gag ctg cga Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr Gly Ala Glu Leu Arg 375 380 385	1688
cac tgg tca gac atg ctg gcc aac ccc cgg cga ccc atc gcc cag tgg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro Ile Ala Gln Trp 390 395 400	1736
cac act ctg cag gta gag gag gag gtt gat gcc atg ctg gct gtc aag His Thr Leu Gln Val Glu Glu Glu Val Asp Ala Met Leu Ala Val Lys 405 410 415 420	1784
aag taa aggggaaaag aagcctttct gcgtctgccc acgtagtgtct ctttagccag Lys	1840
tatctgtaaa tacctcagta atatgggtcc tttcagtttc cagccatgca ttcctgatac	1900
aatccagtgg tacttcagat cctgtttttaa ttgcacaaa ttttaagtgt gaaagcccct	1960
atgcccttca tcataccact gccctccaaa tctactcttc ttttaagcaa tatgatgtgt	2020
agatagagca tgactgaaat gtattgtatc acaccgttgt atataccagt atgctaaaga	2080
tttatttcta gtttgtgtat ttgtatgttg taagcgtttc ctaatctgtg tataatctaga	2140
tgtttttaat aagatgttct attttaaact atgtaaattg actgagatat aggagaactg	2200
ataatatatt atatggtaaa tatagtatcg tctgcattcc agcaaaaata tcaatttgaa	2260
aggcactagt acagttaaac caacatctta aaggacaact taaacctgaa ctttctattg	2320
aatcctttga gtaccaagat ttgctcacac gacatctttg atgggtgaac ccaattttgt	2380

a

2381

<210> 2
 <211> 421
 <212> PRT
 <213> Mus musculus

<400> 2

Met Val Ser Ala Ser Arg Pro Glu Ala Leu Ala Ala Pro Val Thr Thr
 1 5 10 15

Val Ala Thr Leu Val Pro His Asn Ala Thr Glu Pro Ala Ser Pro Gly
 20 25 30

Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Gln Lys Phe Met Asn
 35 40 45

Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala
 50 55 60

Ile Val Ala Val Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys
 65 70 75 80

Lys Cys Leu Phe Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly
 85 90 95

Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr
 100 105 110

Met Lys Asp Gln Ala Leu Lys Asp Asp Ala Glu Thr Gly Leu Thr
 115 120 125

Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Glu Lys Leu Gly Lys
 130 135 140

Leu Gln Tyr Ser Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val
 145 150 155 160

Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr
 165 170 175

Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys
 180 185 190

Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu
 195 200 205

Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu

210 215 960296_99004_Seq_Lst
220

Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile
225 230 235 240

Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr
245 250 255

Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys
260 265 270

Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys
275 280 285

Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val
290 295 300

Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly
305 310 315 320

Lys Arg Leu Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn
325 330 335

Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile
340 345 350

Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly
355 360 365

Lys Asn Asp Ala Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr Gly
370 375 380

Ala Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro
385 390 395 400

Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala Met
405 410 415

Leu Ala Val Lys Lys
420

<210> 3
<211> 4654
<212> DNA
<213> Rattus rattus

<220>
<221> CDS

960296_99004_Seq_Lst

<222> (526)..(1791)

<220>
 <221> misc_feature
 <222> (619)..(681)
 <223> BoNT/B binding domain

<220>
 <221> misc_feature
 <222> (682)..(762)
 <223> Gangliosides binding domain or transmembrane domain

<400> 3

ctctgaccga gttcagcccc cagtgtcttt cctccacctc ctctgcagc ggcagcatcg	60
gcagttggca gtgggcaact tgaggctgta accagggcaa gccccaggg tcctgctcac	120
ccgacagggg gctcagctcc ccaaaggggt gtgtgcaggg cgggggcggc cagctgggac	180
cagctggtgg ccctagaaaa cctcaccac acccacacac cccttttgtg ttgcaggctg	240
cccctctgag agcggaggca gcgagagtac tcgcgtgcct cgcaccggtc cgcggtgaga	300
gctgcgggga ccaagactcg caccacctcc cggtcctcgc tccaggaaaa gaagacttga	360
aagtgcttga gcaaccaaca tccgcagtca gatcggaaga ctctgccctg gccatcccca	420
gagcgccacc agaacgtctc attaagattg aagaaagatt ccgagaagaa caaaaccccc	480
caaatactcc ataataccct gcagaacatt tcacttgaac caaaa atg gtg agt gcc	537
Met Val Ser Ala	
1	
agt cat cct gag gcc ctg gcc gcc cct gtc acc act gtt gcg acc ctt	585
Ser His Pro Glu Ala Leu Ala Ala Pro Val Thr Thr Val Ala Thr Leu	
5 10 15 20	
gtc cca cac aat gcc act gag cca gcc agt cct ggg gaa ggg aag gaa	633
Val Pro His Asn Ala Thr Glu Pro Ala Ser Pro Gly Glu Gly Lys Glu	
25 30 35	
gat gcc ttt tcc aag ctg aag cag aag ttt atg aat gag ctg cat aaa	681
Asp Ala Phe Ser Lys Leu Lys Gln Lys Phe Met Asn Glu Leu His Lys	
40 45 50	
att cca ttg cca ccg tgg gcc tta ata gcc ata gcc ata gtt gcg gtc	729
Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala Ile Val Ala Val	
55 60 65	
ctt tta gtc gta acc tgc tgc ttt tgt gtc tgt aag aaa tgt ttg ttc	777
Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys Lys Cys Leu Phe	
70 75 80	
aaa aag aaa aac aag aag aag ggg aag gaa aag gga gga aag aac gcc	825
Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly Gly Lys Asn Ala	
85 90 95 100	
att aac atg aaa gac gtg aaa gac tta ggg aag acc atg aag gat cag	873
Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr Met Lys Asp Gln	
105 110 115	
gcc ctt aag gat gac gat gct gaa acc gga ctg act gat gga gaa gaa	921
Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu Thr Asp Gly Glu Glu	

960296_99004_Seq_Lst																
120					125					130						
aag Lys	gaa Glu	gag Glu 135	ccc Pro	aag Lys	gaa Glu	gag Glu 140	gag Glu 140	aaa Lys	ctg Leu	gga Gly	aag Lys	ctc Leu 145	caa Gln	tat Tyr	tca Ser	969
ctg Leu	gac Asp 150	tat Tyr	gac Asp	ttc Phe	cag Gln	aat Asn 155	aac Asn	cag Gln	ctg Leu	ttg Leu	gtg Val 160	gga Gly	atc Ile	atc Ile	cag Gln	1017
gct Ala 165	gct Ala	gaa Glu	ctg Leu	ccc Pro	gcc Ala 170	ctg Leu	gac Asp	atg Met	ggg Gly	ggt Gly 175	aca Thr	tcc Ser	gat Asp	cca Pro	tac Tyr 180	1065
gtc Val	aaa Lys	gtc Val	ttc Phe	ctg Leu 185	ctg Leu	cct Pro	gaa Glu	aaa Lys	aag Lys 190	aag Lys	aaa Lys	ttt Phe	gag Glu 195	act Thr 195	aaa Lys	1113
gtc Val	cac His	cgg Arg	aaa Lys 200	acc Thr	ctc Leu	aat Asn	cca Pro	gtc Val 205	ttc Phe	aat Asn	gaa Glu	caa Gln	ttt Phe 210	act Thr	ttc Phe	1161
aag Lys	gta Val	ccc Pro 215	tac Tyr	tcg Ser	gaa Glu	tta Leu	ggt Gly 220	ggc Gly	aaa Lys	acc Thr	ctg Leu	gtg Val 225	atg Met	gct Ala	gtg Val	1209
tat Tyr	gac Asp 230	ttt Phe	gat Asp	cgc Arg	ttc Phe	tcc Ser 235	aag Lys	cac His	gac Asp	atc Ile	atc Ile 240	gga Gly	gag Glu	ttc Phe	aaa Lys	1257
gtt Val 245	cct Pro	atg Met	aac Asn	acc Thr	gtg Val 250	gat Asp	ttt Phe	ggc Gly	cat His	gtg Val 255	acc Thr	gag Glu	gag Glu	tgg Trp	cgc Arg 260	1305
gat Asp	ctc Leu	cag Gln	agc Ser	gct Ala 265	gag Glu	aaa Lys	gaa Glu	gag Glu	caa Gln 270	gag Glu	aaa Lys	ctg Leu	ggt Gly	gac Asp 275	atc Ile	1353
tgc Cys	ttc Phe	tcc Ser	ctc Leu 280	cgc Arg	tac Tyr	gtc Val	cct Pro	act Thr 285	gcc Ala	ggc Gly	aaa Lys	ctg Leu	act Thr 290	gtt Val	gtc Val	1401
att Ile	ctg Leu	gaa Glu 295	gcc Ala	aag Lys	aac Asn	ctg Leu	aag Lys 300	aag Lys	atg Met	gat Asp	gtg Val	ggt Gly 305	ggc Gly	tta Leu	tct Ser	1449
gat Asp	ccc Pro 310	tac Tyr	gtg Val	aag Lys	att Ile	cac His 315	ctg Leu	atg Met	cag Gln	aac Asn	ggt Gly 320	aag Lys	agg Arg	ctg Leu	aag Lys	1497
aag Lys 325	aaa Lys	aag Lys	acg Thr	acg Thr	att Ile 330	aag Lys	aag Lys	aac Asn	aca Thr	ctc Leu 335	aac Asn	ccc Pro	tac Tyr	tac Tyr	aac Asn 340	1545
gag Glu	tcc Ser	ttc Phe	agc Ser	ttt Phe 345	gaa Glu	gtt Val	ccg Pro	ttc Phe	gag Glu 350	caa Gln	atc Ile	cag Gln	aaa Lys	gtg Val 355	caa Gln	1593
gtg Val	gtg Val	gta Val	act Thr 360	gtt Val	ttg Leu	gac Asp	tat Tyr	gac Asp 365	aag Lys	att Ile	ggc Gly	aag Lys	aac Asn 370	gac Asp	gcc Ala	1641
atc	gac	aaa	gtc	ttc	gtt	ggt	tac	aac	agc	act	ggg	gcg	gag	ctg	cga	1689

960296_99004_Seq_Lst

Ile	Asp	Lys	Val	Phe	Val	Gly	Tyr	Asn	Ser	Thr	Gly	Ala	Glu	Leu	Arg	
		375					380					385				
cac	tgg	tca	gac	atc	ctg	gcc	aac	ccc	cgg	cga	ccc	atc	gca	cag	tgg	1737
His	Trp	Ser	Asp	Ile	Leu	Ala	Asn	Pro	Arg	Arg	Pro	Ile	Ala	Gln	Trp	
	390					395					400					
cac	act	ctg	cag	gta	gag	gag	gag	gtt	gat	gcc	atg	ctg	gct	gtc	aag	1785
His	Thr	Leu	Gln	Val	Glu	Glu	Glu	Val	Asp	Ala	Met	Leu	Ala	Val	Lys	
405					410					415					420	
aag	taa	agggaaaacg	aagcctttct	gcattctgccc	acatagtgct	ctttagccag										1841
Lys																
tatctgtaaa	tacctcagta	atatgggtcc	ttttggtttc	cagccatgca	ttcctgatac											1901
aatccagtgg	tacttcaa	cctgttttaa	tttgcacaaa	tttaagtgt	gaaagccctt											1961
atgccctcca	tcataccact	gccctccaaa	tctactcttc	ttttaagcaa	tatgatgtgt											2021
agatagagca	tgactgaaat	tatgtattgt	atcacactgt	tgtatatacc	agtatgctaa											2081
agattttatt	ctagtttgtg	tatttgtatg	ttgtaagcgt	ttcctaacct	gtgtatatct											2141
agatgttttt	aataagatgt	cctattttta	actatgtaaa	ttgactgaga	tatagagctg											2201
ataatatatt	atatggtaaa	tatagtatcg	tgtgcattcc	agcaaaaata	tcaacttgaa											2261
aggcactagt	acagttaa	caacatctta	aaggacaact	taaacctgag	ctttctattg											2321
aatcctttga	gtaccaagat	tcgctcacac	aacacctttg	atgggcgaac	ccaattttgt											2381
agaattcttt	cacaggcaaa	tagcatgacc	tgagcagcat	ctgggctgac	ctcaaggaag											2441
caaagccaca	aaccagaata	gcattctgtct	gtctgtacct	gcaaagccaa	agccatgctt											2501
cgctcttaca	gtcaaggaag	caatgaacag	gagccaatgc	gttcctacca	ctgcatctag											2561
catagcttca	tgggtggtgt	ctctgtgtgt	gcgtgtgcaa	gcgtgaaagt	gtatgcacgt											2621
gtgtatgtgt	ggtgcatgcc	tttgtttggg	gttaggggtgg	gggaggagga	gctgagggaa											2681
gtcagcgttt	ctgaaatatt	gcctgcctgt	ttaaacagaa	aattatagct	ctccattgtc											2741
acatttatat	aaaacgtgca	acctgggaat	tctgatccgg	atttcacccc	aatattgatt											2801
ccaaaaggta	ttcgcgtgag	actttgtaac	aaaatatttt	attatacaaa	accagattag											2861
aaggaatgca	gaatattttt	aacgcagcaa	tctgtgctta	ttccacaaag	tgactttgtg											2921
gtaaacagac	agtattgtaa	ccccacgaaa	agacggaata	taacagttag	ccatagttct											2981
gaatgcactt	cgacgaagcc	aaaacagaca	gctagtgatc	tttttatatg	ctctttttac											3041
gtgagtttta	atttgtcctt	taaacaaagg	tgaaacaaaa	ccaagaacaa	gttctcgcaa											3101
actgaagcaa	cctcttatgt	acactagatg	cttgacttag	gaggagtttt	taaatgttct											3161
caatgttatt	ctgtagtaaa	tggcactatt	atgaagccac	tagtcattcc	atatgagtct											3221
taaggacggc	tctgtgtaac	actgtgactg	ccccgtgtgc	ttagacacgt	agtttcctca											3281

960296_99004_Seq_Lst

gtggatagca	ctcaacttac	tccgtagtga	tattgtgaaca	atactgccat	tccctcttac	3341
tgcactgccc	aacatgtgtg	tagcacaaaac	agttctcatt	cctaaggacc	aattcagaac	3401
tgaacagcta	tgcataggac	agaaagatac	atagaccggg	tgtgggagaa	cacacagcat	3461
tttgtcaaca	ctgtgcacta	gtcacatttg	tcctgctgcc	ggtagacagc	cacttcagga	3521
agtgagcctg	ctacctaaca	ccgcttctag	actcttctcc	cacttgctat	tgtggcccgt	3581
tttcacctcc	aggtcacaga	gaatggcaac	atcctgaagg	gagagaccat	cttcacatct	3641
accaaaaataa	aatggaggaa	tgctaagcat	ggcctcgtgc	ttgatcttta	ggaattagct	3701
ccgtgttttg	gacaaaactc	aagagaatcc	ccaatagggc	tggtggtaga	ctttaagcac	3761
ggggtcggct	gctcctcctg	cacacacaac	acaaaagcta	acccctgggt	gtgattcttc	3821
cctcatgaga	gaagaggcaa	accctttgcc	cttcactccc	atcacagcaa	actttcagac	3881
ctagaacaga	cacacaggac	aaggagcaaa	tccttcccta	tggatgaaca	gcacgtttcc	3941
aacattaaaa	ccacagatga	taggaaacac	atactcatag	gtgagttaaa	cagcagttta	4001
aacaggagac	tcaaagtagg	ggctttccta	tctaagggat	caagtcctac	caaagagaag	4061
gaacacctta	aataccagac	actgacattt	aatttcatca	tctcccgact	tgagttgtac	4121
acaatggaac	atttccgagg	acgcagctcc	gagctgccga	actgacatta	cttcctgcat	4181
tacaatgata	ctagcacatt	ctcttgcaac	actgccaaca	tgggattgtc	accatagagt	4241
tagttggtac	tatatcattc	tcttgtgagc	cggtgactgg	acctgctttc	tgaccaagat	4301
ccatcctctg	ataagccaca	tgtacctttc	tgacaatgca	gtgtgaagtc	ttagaagctg	4361
atgccctaga	aagatcctag	ttgcctttgt	gtatacttac	tgcttgcttg	agtgtttcta	4421
tgtgtggatt	ttctctgtgt	ctggtagaaa	tgttgggggtg	ttttcttctg	ccataaggct	4481
tgtgaccgc	gagccaattc	ccttagctgt	actttccctt	cattttttga	taagtggttt	4541
aaattctggt	tcactttgtg	tagtgaacct	catggtagtt	ttctgattgt	tgttaaaaaa	4601
aatgacttaa	catattacat	ggacactcaa	taaaaatggt	ttatttcctg	tta	4654

<210> 4
 <211> 421
 <212> PRT
 <213> Rattus rattus

<400> 4

Met	Val	Ser	Ala	Ser	His	Pro	Glu	Ala	Leu	Ala	Ala	Pro	Val	Thr	Thr
1				5					10					15	

Val	Ala	Thr	Leu	Val	Pro	His	Asn	Ala	Thr	Glu	Pro	Ala	Ser	Pro	Gly
			20					25					30		

Glu	Gly	Lys	Glu	Asp	Ala	Phe	Ser	Lys	Leu	Lys	Gln	Lys	Phe	Met	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35 960296_99004_Seq_Lst
 40 45
 Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala
 50 55 60
 Ile Val Ala Val Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys
 65 70 75 80
 Lys Cys Leu Phe Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly
 85 90 95
 Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr
 100 105 110
 Met Lys Asp Gln Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu Thr
 115 120 125
 Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Glu Lys Leu Gly Lys
 130 135 140
 Leu Gln Tyr Ser Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val
 145 150 155 160
 Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr
 165 170 175
 Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Glu Lys Lys Lys Lys
 180 185 190
 Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu
 195 200 205
 Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu
 210 215 220
 Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile
 225 230 235 240
 Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr
 245 250 255
 Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys
 260 265 270
 Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys
 275 280 285

960296_99004_Seq_Lst

Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val
 290 295 300

Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly
 305 310 315 320

Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn
 325 330 335

Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile
 340 345 350

Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly
 355 360 365

Lys Asn Asp Ala Ile Asp Lys Val Phe Val Gly Tyr Asn Ser Thr Gly
 370 375 380

Ala Glu Leu Arg His Trp Ser Asp Ile Leu Ala Asn Pro Arg Arg Pro
 385 390 395 400

Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala Met
 405 410 415

Leu Ala Val Lys Lys
 420

<210> 5
 <211> 422
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (33)..(53)
 <223> BoNT/B binding domain

<220>
 <221> MISC_FEATURE
 <222> (54)..(80)
 <223> Gangliosides binding domain or transmembrane domain

<400> 5

Met Val Ser Glu Ser His His Glu Ala Leu Ala Ala Pro Pro Val Thr
 1 5 10 15

Thr Val Ala Thr Val Leu Pro Ser Asn Ala Thr Glu Pro Ala Ser Pro
 20 25 30

Gly Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Glu Lys Phe Met

960296_99004_Seq_Lst

35 40 45
 Asn Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile
 50 55 60
 Ala Ile Val Ala Val Leu Leu Val Leu Thr Cys Cys Phe Cys Ile Cys
 65 70 75 80
 Lys Lys Cys Leu Phe Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys
 85 90 95
 Gly Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys
 100 105 110
 Thr Met Lys Asp Gln Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu
 115 120 125
 Thr Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Glu Lys Leu Gly
 130 135 140
 Lys Leu Gln Tyr Ser Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu
 145 150 155 160
 Val Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
 165 170 175
 Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
 180 185 190
 Lys Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn
 195 200 205
 Glu Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr
 210 215 220
 Leu Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile
 225 230 235 240
 Ile Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val
 245 250 255
 Thr Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu
 260 265 270
 Lys Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly
 275 280 285

960296_99004_Seq_Lst

Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp
 290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn
 305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu
 325 330 335

Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln
 340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile
 355 360 365

Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr
 370 375 380

Gly Ala Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg
 385 390 395 400

Pro Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala
 405 410 415

Met Leu Ala Val Lys Lys
 420

<210> 6
 <211> 1876
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (16)..(1284)

<220>
 <221> misc_feature
 <222> (133)..(195)
 <223> BONT/B binding domain

<220>
 <221> misc_feature
 <222> (196)..(276)
 <223> Gangliosides binding domain or transmembrane domain

<400> 6
 atccccctctg ccacc atg aga aac atc ttc aag agg aac cag gag cca aat 51
 Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Asn
 1 5 10

gtg gct ccg gcc acc acc act gcc aca atg ccc ctt gca ccc gtc gca 99
 Val Ala Pro Ala Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Val Ala

960296_99004_Seq_Lst																
15					20					25						
cct	gcc	gac	aac	tct	aca	gag	agc	acg	ggt	cct	ggg	gag	agc	caa	gaa	147
Pro	Ala	Asp	Asn	Ser	Thr	Glu	Ser	Thr	Gly	Pro	Gly	Glu	Ser	Gln	Glu	
	30					35					40					
gac	atg	ttc	gcc	aag	ctg	aag	gag	aaa	ttc	ttc	aat	gag	atc	aac	aag	195
Asp	Met	Phe	Ala	Lys	Leu	Lys	Glu	Lys	Phe	Phe	Asn	Glu	Ile	Asn	Lys	
45					50					55					60	
atc	ccc	ttg	ccc	ccc	tgg	gct	ctg	atc	gcc	atg	gct	gtg	gtt	gct	ggc	243
Ile	Pro	Leu	Pro	Pro	Trp	Ala	Leu	Ile	Ala	Met	Ala	Val	Val	Ala	Gly	
				65					70					75		
ctc	ctg	ctg	ctc	acc	tgt	tgc	ttc	tgc	atc	tgt	aag	aag	tgc	tgc	tgc	291
Leu	Leu	Leu	Leu	Thr	Cys	Cys	Phe	Cys	Ile	Cys	Lys	Lys	Cys	Cys	Cys	
			80					85					90			
aag	aag	aag	aag	aac	aag	aag	gag	aag	ggc	aaa	ggc	atg	aag	aac	gcc	339
Lys	Lys	Lys	Lys	Asn	Lys	Lys	Glu	Lys	Gly	Lys	Gly	Met	Lys	Asn	Ala	
		95					100					105				
atg	aac	atg	aag	gac	atg	aaa	ggg	ggc	cag	gat	gac	gat	gat	gca	gag	387
Met	Asn	Met	Lys	Asp	Met	Lys	Gly	Gly	Gln	Asp	Asp	Asp	Asp	Ala	Glu	
	110					115					120					
aca	ggc	ctg	act	gaa	gga	gaa	ggt	gaa	ggc	gag	gag	gag	aaa	gag	cca	435
Thr	Gly	Leu	Thr	Glu	Gly	Glu	Gly	Glu	Gly	Glu	Glu	Glu	Lys	Glu	Pro	
125					130					135					140	
gag	aac	ctg	ggc	aaa	ttg	cag	ttt	tct	ctg	gac	tat	gat	ttc	cag	gcc	483
Glu	Asn	Leu	Gly	Lys	Leu	Gln	Phe	Ser	Leu	Asp	Tyr	Asp	Phe	Gln	Ala	
				145					150					155		
aac	cag	ctc	acc	gtg	ggt	gtc	ctg	cag	gct	gcg	gaa	ctc	cca	gcc	ctg	531
Asn	Gln	Leu	Thr	Val	Gly	Val	Leu	Gln	Ala	Ala	Glu	Leu	Pro	Ala	Leu	
			160					165					170			
gac	atg	ggt	ggc	aca	tca	gac	cct	tat	gtc	aaa	gtc	ttc	ctc	ctc	cca	579
Asp	Met	Gly	Gly	Thr	Ser	Asp	Pro	Tyr	Val	Lys	Val	Phe	Leu	Leu	Pro	
		175					180					185				
gac	aag	aag	aag	aaa	tat	gag	act	aag	gtg	cat	cgg	aag	acg	ctg	aac	627
Asp	Lys	Lys	Lys	Lys	Tyr	Glu	Thr	Lys	Val	His	Arg	Lys	Thr	Leu	Asn	
	190					195					200					
cca	gcc	ttc	aat	gag	aca	ttc	act	ttc	aag	gtg	cca	tac	cag	gag	tta	675
Pro	Ala	Phe	Asn	Glu	Thr	Phe	Thr	Phe	Lys	Val	Pro	Tyr	Gln	Glu	Leu	
205					210					215					220	
gca	ggc	aag	acc	ctg	gtg	atg	gca	atc	tat	gac	ttt	gac	cgc	ttc	tct	723
Ala	Gly	Lys	Thr	Leu	Val	Met	Ala	Ile	Tyr	Asp	Phe	Asp	Arg	Phe	Ser	
				225					230					235		
aag	cat	gac	atc	atc	ggg	gag	gtg	aag	gta	ccc	atg	aac	aca	gtg	gac	771
Lys	His	Asp	Ile	Ile	Gly	Glu	Val	Lys	Val	Pro	Met	Asn	Thr	Val	Asp	
			240					245					250			
ctt	ggc	cag	ccc	atc	gag	gaa	tgg	aga	gac	cta	caa	ggc	gga	gag	aag	819
Leu	Gly	Gln	Pro	Ile	Glu	Glu	Trp	Arg	Asp	Leu	Gln	Gly	Gly	Glu	Lys	
		255					260					265				
gaa	gag	cca	gag	aag	ttg	ggt	gac	atc	tgt	acc	tcc	ttg	cgc	tac	gtg	867

960296_99004_Seq_Lst

Glu	Glu	Pro	Glu	Lys	Leu	Gly	Asp	Ile	Cys	Thr	Ser	Leu	Arg	Tyr	Val		
270						275					280						
ccc	aca	gct	ggg	aag	ctc	acc	gtc	tgt	atc	ctg	gag	gcc	aag	aac	ctg	915	
Pro	Thr	Ala	Gly	Lys	Leu	Thr	Val	Cys	Ile	Leu	Glu	Ala	Lys	Asn	Leu		
285					290					295					300		
aag	aag	atg	gac	gta	ggg	ggc	ctt	tca	gac	ccc	tat	gtg	aag	atc	cac	963	
Lys	Lys	Met	Asp	Val	Gly	Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Ile	His		
				305					310					315			
ctg	atg	cag	aac	ggt	aag	aga	ctc	aag	aag	aag	aag	acg	aca	gtg	aag	1011	
Leu	Met	Gln	Asn	Gly	Lys	Arg	Leu	Lys	Lys	Lys	Lys	Thr	Thr	Val	Lys		
			320					325					330				
aag	aag	acc	ctg	aac	ccc	tac	ttc	aac	gag	tcc	ttc	agc	ttc	gag	atc	1059	
Lys	Lys	Thr	Leu	Asn	Pro	Tyr	Phe	Asn	Glu	Ser	Phe	Ser	Phe	Glu	Ile		
		335					340					345					
ccc	ttt	gag	cag	atc	cag	aaa	gtc	cag	gtg	gtc	gtc	acc	gtg	cta	gac	1107	
Pro	Phe	Glu	Gln	Ile	Gln	Lys	Val	Gln	Val	Val	Val	Thr	Val	Leu	Asp		
	350					355					360						
tac	gac	aaa	ctg	ggc	aag	aat	gaa	gcc	atc	gga	aag	atc	ttt	gta	ggc	1155	
Tyr	Asp	Lys	Leu	Gly	Lys	Asn	Glu	Ala	Ile	Gly	Lys	Ile	Phe	Val	Gly		
365				370						375					380		
agc	aac	gcc	aca	ggc	acc	gag	ttg	cgg	cac	tgg	tcc	gac	atg	ctg	gcc	1203	
Ser	Asn	Ala	Thr	Gly	Thr	Glu	Leu	Arg	His	Trp	Ser	Asp	Met	Leu	Ala		
				385					390					395			
aac	cct	cgg	agg	ccc	att	gcc	cag	tgg	cac	tct	ctt	aag	cct	gag	gaa	1251	
Asn	Pro	Arg	Arg	Pro	Ile	Ala	Gln	Trp	His	Ser	Leu	Lys	Pro	Glu	Glu		
			400					405					410				
gaa	gtg	gat	gct	ctt	ctg	ggc	aag	aac	aag	tag	gctccagcgg	ccggtgccac	1304				
Glu	Val	Asp	Ala	Leu	Leu	Gly	Lys	Asn	Lys								
		415				420											
gccccctaagg	agccacgccc	ccgaggcgcc	acgccccctg	aggacactga	cgagatccag	1364											
agctatcaat	acctcagtta	cgcgacctta	gaggttttctt	catttgtttg	cggtgtgtcc	1424											
tgtttttctt	tcctttttct	ctttttaaaag	accaacttcc	ttttggtggc	tgtgtgaaga	1484											
gagtccccta	agaggtgaaa	gaaaagcctg	gctctgttat	tgtccccgga	gcggtccttg	1544											
ttgcatgccc	tttcacgggt	tcccccttac	cccaagtggg	gccctctact	gtcagacagt	1604											
tgaagcacta	actgcttttc	ctgggttttg	gaccaacaac	atggcaagca	cattctgttt	1664											
cttgactgtg	aaggcaacat	agtggccagc	atttgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	1724											
tatgtgtgtg	tgtacacctg	tatgtgcca	tccatcccca	cctgcctgtt	ttgaacatct	1784											
ctcttcattt	tctggaatga	gtcatggaca	gtgaagccat	gtgagaggag	aatgtcttca	1844											
gagactccaa	gggaaagcaa	gcccactgcc	tg			1876											

<210> 7
 <211> 422
 <212> PRT

960296_99004_Seq_Lst

<213> Mus musculus

<400> 7

```

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Asn Val Ala Pro Ala
1      5      10      15

Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Val Ala Pro Ala Asp Asn
20      25      30

Ser Thr Glu Ser Thr Gly Pro Gly Glu Ser Gln Glu Asp Met Phe Ala
35      40      45

Lys Leu Lys Glu Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro
50      55      60

Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu
65      70      75      80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys
85      90      95

Asn Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys
100     105     110

Asp Met Lys Gly Gly Gln Asp Asp Asp Ala Glu Thr Gly Leu Thr
115     120     125

Glu Gly Glu Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly
130     135     140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr
145     150     155     160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
165     170     175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
180     185     190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn
195     200     205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Ala Gly Lys Thr
210     215     220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile
225     230     235     240

```


960296_99004_Seq_Lst

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln
340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr
370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg
385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala
405 410 415

Leu Leu Gly Lys Asn Lys
420

<210> 8
<211> 2681
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (115)..(1383)

<220>
<221> misc_feature
<222> (232)..(294)
<223> BoNT/B binding domain

960296_99004_Seq_Lst

<220>

<221> misc_feature

<222> (295)..(375)

<223> Gangliosides binding domain or transmembrane domain

<400> 8

gggagccgat cggtgtgggc tggtggagaa ggcagcggga gtctgccgcc ccgaagtcca 60

ggtccctctt tccactccc gcgccggcca gcgctgcggc tccctctgc cacc atg 117
Met
1

aga aac atc ttc aag agg aac cag gag ccc att gtg gct ccg gcc acc 165
Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala Thr
5 10 15

acc act gcc aca atg cct ctg gca ccc gcc gca cct gcc gat aac tct 213
Thr Thr Ala Thr Met Pro Leu Ala Pro Ala Ala Pro Ala Asp Asn Ser
20 25 30

aca gag agc acg ggc acc ggg gag agc caa gaa gac atg ttc gcc aag 261
Thr Glu Ser Thr Gly Thr Gly Glu Ser Gln Glu Asp Met Phe Ala Lys
35 40 45

ctg aag gac aaa ttc ttc aat gag atc aac aag atc cct ttg ccc ccc 309
Leu Lys Asp Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro
50 55 60 65

tgg gct ctg att gcc atg gcc gtg gtt gct ggc ctc ctg ctg ctc acc 357
Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu Thr
70 75 80

tgc tgc ttc tgc atc tgt aag aag tgc tgc tgc aag aag aag aaa aac 405
Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys Asn
85 90 95

aag aag gag aag ggc aaa ggc atg aag aac gcc atg aac atg aag gac 453
Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys Asp
100 105 110

atg aag ggg ggc cag gat gat gac gac gcg gag aca ggc ctg act gaa 501
Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr Glu
115 120 125

gga gaa gga gaa ggc gag gag gag aaa gag ccg gag aac ctg ggc aaa 549
Gly Glu Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly Lys
130 135 140 145

ttg cag ttt tct ctg gac tat gat ttc caa gcc aac cag ctc acc gtg 597
Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val
150 155 160

ggc gtc ctg cag gct gct gaa ctc ccg gcc ctg gac atg ggt ggc acg 645
Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr
165 170 175

tca gac cct tac gtc aaa gtc ttc ctc ctc cca gac aag aag aag aaa 693
Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys
180 185 190

tat gag acc aag gtg cac cgg aag aca ctg aac cca gcc ttc aac gaa 741
Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu

960296_99004_Seq_Lst																
195					200					205						
act	ttc	act	ttc	aag	gtg	cca	tac	cag	gag	tta	gga	ggc	aaa	acc	ctg	789
Thr	Phe	Thr	Phe	Lys	Val	Pro	Tyr	Gln	Glu	Leu	Gly	Gly	Lys	Thr	Leu	
210					215					220					225	
gtg	atg	gct	atc	tat	gac	ttt	gac	cgc	ttc	tct	aag	cat	gac	atc	atc	837
Val	Met	Ala	Ile	Tyr	Asp	Phe	Asp	Arg	Phe	Ser	Lys	His	Asp	Ile	Ile	
				230					235					240		
ggg	gag	gtg	aaa	gtg	ccc	atg	aac	acg	gtg	gac	ctt	ggc	cag	ccc	atc	885
Gly	Glu	Val	Lys	Val	Pro	Met	Asn	Thr	Val	Asp	Leu	Gly	Gln	Pro	Ile	
			245					250					255			
gag	gaa	tgg	aga	gac	cta	caa	ggc	gga	gag	aag	gaa	gag	cca	gag	aag	933
Glu	Glu	Trp	Arg	Asp	Leu	Gln	Gly	Gly	Glu	Lys	Glu	Glu	Pro	Glu	Lys	
		260					265					270				
ctg	ggt	gac	atc	tgt	acc	tcc	ttg	cgc	tac	gtg	ccc	act	gct	ggg	aag	981
Leu	Gly	Asp	Ile	Cys	Thr	Ser	Leu	Arg	Tyr	Val	Pro	Thr	Ala	Gly	Lys	
	275					280					285					
ctc	acc	gtc	tgt	atc	ctg	gag	gcc	aag	aac	ctg	aag	aag	atg	gat	gtg	1029
Leu	Thr	Val	Cys	Ile	Leu	Glu	Ala	Lys	Asn	Leu	Lys	Lys	Met	Asp	Val	
					295					300					305	
ggg	ggc	ctc	tca	gac	ccc	tat	gtg	aag	atc	cac	ttg	atg	cag	aat	ggc	1077
Gly	Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Ile	His	Leu	Met	Gln	Asn	Gly	
				310					315					320		
aag	aga	ctc	aag	aag	aag	aag	acg	acg	gtg	aag	aag	aag	acc	ttg	aac	1125
Lys	Arg	Leu	Lys	Lys	Lys	Lys	Thr	Thr	Val	Lys	Lys	Lys	Thr	Leu	Asn	
			325					330					335			
ccc	tac	ttc	aat	gag	tca	ttc	agc	ttc	gag	atc	ccc	ttt	gag	cag	atc	1173
Pro	Tyr	Phe	Asn	Glu	Ser	Phe	Ser	Phe	Glu	Ile	Pro	Phe	Glu	Gln	Ile	
		340					345					350				
cag	aaa	gtc	cag	gtg	gtc	gtc	acc	gtg	cta	gac	tat	gac	aaa	ctg	ggc	1221
Gln	Lys	Val	Gln	Val	Val	Val	Thr	Val	Leu	Asp	Tyr	Asp	Lys	Leu	Gly	
	355					360					365					
aag	aat	gaa	gcc	atc	gga	aag	atc	ttc	gta	ggc	agc	aac	gct	aca	ggc	1269
Lys	Asn	Glu	Ala	Ile	Gly	Lys	Ile	Phe	Val	Gly	Ser	Asn	Ala	Thr	Gly	
					375					380					385	
acg	gag	ctg	cgg	cac	tgg	tcc	gac	atg	ctg	gcg	aac	cct	cgg	agg	ccc	1317
Thr	Glu	Leu	Arg	His	Trp	Ser	Asp	Met	Leu	Ala	Asn	Pro	Arg	Arg	Pro	
				390					395					400		
atc	gcc	cag	tgg	cac	tct	ctg	aag	cct	gag	gaa	gaa	gtg	gat	gct	ctt	1365
Ile	Ala	Gln	Trp	His	Ser	Leu	Lys	Pro	Glu	Glu	Glu	Val	Asp	Ala	Leu	
			405					410					415			
ctg	ggc	aag	aac	aag	tag	gcagcggcgc	ctggggccac	gccccagagg								1413
Leu	Gly	Lys	Asn	Lys												
		420														
acactgacga	gctccagagc	tatcaataacc	tcagttatgc	gaccttagag	gtttcttcat											1473
ttgtttgcgg	tgtgtcctgt	tttcctttcc	tttttctttt	tttgtctttt	taaaaaccaa											1533
cttccttttg	gtggctatgt	gaagaggccc	ctaagacgtg	aaagagaagc	ctggctctgt											1593

960296_99004_Seq_Lst

tattgtccca	ggagctgtcc	ttgttgcacg	ccctatcacg	gttgcccctc	accccaagtg	1653
gggccctcta	ctgtcagagt	ggaagcactt	cctgcttttc	ctgggttttg	gaccaacaaa	1713
gtggcaagca	cattctgtgt	ctcgactgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	1773
tgtgtgtgtg	tgtgtgtgta	cacgtgtgcc	catccatccc	caccttgcct	ctgtttggaa	1833
tatctcttcg	tttctggaat	gagtcacgga	caatgatgcc	gtgtgagaga	ggaaagtctt	1893
caggtactcc	gaggtgagga	gagcccactg	cttaagtggg	cagaggccag	aagctctcat	1953
agtccttgcg	aaaggccatt	tggaagacgc	aagatgtgat	actggatgta	ttccgaacta	2013
ggaccaaagg	cttgatgcca	tcccagactc	cctcttgta	gtcatggctt	ccccaggagt	2073
ggggctttgg	gatcattcat	gaaaataaac	tatttactcg	actggtcgga	ttcagccagg	2133
gaccgccagc	tccaggatgt	cattcttggt	gacgacatca	aactttgaag	aaacagaagt	2193
cccattactc	agctctggat	ctttgcctcg	tccagtggga	ggcagatgct	tcctccctct	2253
gcagagtaca	agcagtgcgt	tcatttgcat	tcacgcacca	tctgcttttg	cctctgtttc	2313
cctttttgtg	taagtggaaa	aataccatct	gacgataagt	gctttgcaca	gagccagaga	2373
cctattagag	ggatgcttgg	gtgttttagt	cccttgaggt	ccaggtaagg	aggaggtgtc	2433
aagaagggga	gcgttggtgg	acagtgacaa	gctagacatt	gcagagctcc	tcacaactcc	2493
tattcctgac	cctctggacc	ctttgaccct	cagtgatggg	agccggagta	gcccaggcag	2553
accttaggag	aggccccgtc	cttcccttcc	ttagacagtt	ttctcagaat	gccaggaaac	2613
acagcgcatt	catttcagat	gggtgggtga	gaaaatgtgc	taaggtttgc	accctatggt	2673
cggaattc						2681

<210> 9
 <211> 422
 <212> PRT
 <213> Rattus norvegicus
 <400> 9

Met	Arg	Asn	Ile	Phe	Lys	Arg	Asn	Gln	Glu	Pro	Ile	Val	Ala	Pro	Ala
1				5				10					15		
Thr	Thr	Thr	Ala	Thr	Met	Pro	Leu	Ala	Pro	Ala	Ala	Pro	Ala	Asp	Asn
			20					25					30		
Ser	Thr	Glu	Ser	Thr	Gly	Thr	Gly	Glu	Ser	Gln	Glu	Asp	Met	Phe	Ala
		35					40					45			
Lys	Leu	Lys	Asp	Lys	Phe	Phe	Asn	Glu	Ile	Asn	Lys	Ile	Pro	Leu	Pro
	50					55					60				

960296_99004_Seq_Lst

Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu
65 70 75 80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys
85 90 95

Asn Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys
100 105 110

Asp Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr
115 120 125

Glu Gly Glu Gly Glu Gly Glu Glu Lys Glu Pro Glu Asn Leu Gly
130 135 140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr
145 150 155 160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
180 185 190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn
195 200 205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr
210 215 220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile
225 230 235 240

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn
305 310 315 320

960296_99004_Seq_Lst

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln
340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr
370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg
385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala
405 410 415

Leu Leu Gly Lys Asn Lys
420

<210> 10
<211> 419
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (37)..(57)
<223> BoNT/B binding domain

<220>
<221> MISC_FEATURE
<222> (58)..(84)
<223> Gangliosides binding domain or transmembrane domain

<400> 10

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Ile Gly Pro Val Asp Asn Ser Thr Glu
20 25 30

Ser Gly Gly Ala Gly Glu Ser Gln Glu Asp Met Phe Ala Lys Leu Lys
35 40 45

Glu Lys Leu Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro Trp Ala
50 55 60

960296_99004_Seq_Lst

Leu Ile Ala Ile Ala Val Val Ala Gly Leu Leu Leu Leu Thr Cys Cys
 65 70 75 80

Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys Asn Lys Lys
 85 90 95

Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys Asp Met Lys
 100 105 110

Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr Glu Gly Glu
 115 120 125

Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly Lys Leu Gln
 130 135 140

Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val
 145 150 155 160

Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp
 165 170 175

Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Tyr Glu
 180 185 190

Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe
 195 200 205

Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met
 210 215 220

Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu
 225 230 235 240

Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu
 245 250 255

Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu Lys Leu Gly
 260 265 270

Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr
 275 280 285

Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly
 290 295 300

Leu Ser Asp Pro Tyr Gly Lys Ile His Leu Met Gln Asn Gly Lys Arg
 305 310 315 320

960296_99004_Seq_Lst

Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu Asn Pro Tyr
 325 330 335

Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile Gln Lys
 340 345 350

Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu Gly Lys Asn
 355 360 365

Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr Gly Thr Glu
 370 375 380

Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro Ile Ala
 385 390 395 400

Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala Leu Leu Gly
 405 410 415

Lys Asn Lys